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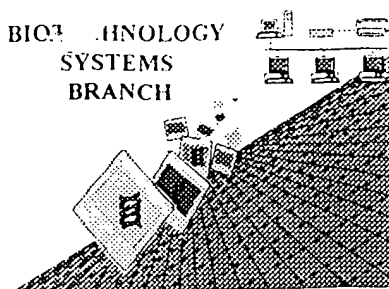
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RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/757,100

Source: OIPE

Date Processed by STIC: 2-5-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/757,100

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ **Wrapped Nucleics** The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☒ **Wrapped Aminos** The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ **Incorrect Line Length** The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ **Misaligned Amino Acid Numbering** The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ **Non-ASCII** This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ **Variable Length** Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ **PatentIn ver. 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ **Skipped Sequences (OLD RULES)** Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ **Skipped Sequences (NEW RULES)** Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ **Use of n's or Xaa's (NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ **Use of <213>Organism (NEW RULES)** Sequence(s) are missing this mandatory field or its response.
- 12 ☐ **Use of <220>Feature (NEW RULES)** Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ **PatentIn ver. 2.0 "bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING DATE: 02/05/2001
 PATENT APPLICATION: US/09/757,100 TIME: 14:24:27

Input Set : A:\isph-533.seq.asc
 Output Set: N:\CRF3\02052001\I757100.raw

6 <110> APPLICANT: Monia, Brett P.
 7 Gaarde, William A.
 8 Nero, Pamela S.
 11 <120> TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
 12 Expression
 14 <130> FILE REFERENCE: ISPH-0533
 C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/757,100
 C--> 17 <141> CURRENT FILING DATE: 2001-01-09
 19 <150> PRIOR APPLICATION NUMBER: 09/377,310
 20 <151> PRIOR FILING DATE: 1999-08-19
 22 <150> PRIOR APPLICATION NUMBER: PCT/US00/18999
 23 <151> PRIOR FILING DATE: 2000-07-13
 25 <160> NUMBER OF SEQ ID NOS: 44
 27 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 3791
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Homo sapiens
 34 <220> FEATURE:
 35 <221> NAME/KEY: CDS
 36 <222> LOCATION: (233)..(3391)
 38 <300> PUBLICATION INFORMATION:
 39 <303> JOURNAL: DNA
 40 <304> VOLUME: 12
 41 <305> ISSUE: 9
 42 <306> PAGES: 823-830
 W--> 43 <307> DATE: 1993-11
 44 <308> DATABASE ACCESSION NO: L13616/Genbank
 45 <309> DATABASE ENTRY DATE: 1995-01-02
 47 <400> SEQUENCE: 1
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 49 gtcgcccagc 60
 E--> 51 gccgccccgt cgtcgtctgc ctctgcttca cggcgccgag ccgcggtccg
 52 agcagaactg 120
 E--> 54 gggtccctt gcattcttca gttacaaatt cagtgccttc tgcagtttcc
 55 ccagagctcc 180
 E--> 57 tcaagaataa cggaaggag aatatgacag atacctagca tctagcaaaa ta
 58 atg gca 238
 60 Met Ala
 62 1
 E--> 64 gct gct tac ctt gac ccc aac ttg aat cac aca cca aat tcg agt
 65 act 286
 66 Ala Ala Tyr Leu Asp Pro Asn Leu Asn His Thr Pro Asn Ser Ser

Does Not Comply
 Corrected Diskette Needed
global errors

wrapped text and
 numbers. see # 1, 2
 on the Error Summary
 sheet.

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/757,100

DATE: 02/05/2001

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Input Set : A:\isph-533.seq.asc

Output Set: N:\CRF3\02052001\I757100.raw

W--> 67 Thr
W--> 68 5 10 15
E--> 70 aag act cac ctg ggt act ggt atg gaa cgt tct cct ggt gca atg
71 gag 334
72 Lys Thr His Leu Gly Thr Gly Met Glu Arg Ser Pro Gly Ala Met
W--> 73 Glu
W--> 74 20 25 30
E--> 76 cga gta tta aag gtc ttt cat tat ttt gaa agc aat agt gag cca
77 acc 382
78 Arg Val Leu Lys Val Phe His Tyr Phe Glu Ser Asn Ser Glu Pro
W--> 79 Thr
W--> 80 35 40 45
E--> 81 50
E--> 83 acc tgg gcc agt att atc agg cat gga gat gct act gat gtc agg
84 ggc 430
85 Thr Trp Ala Ser Ile Ile Arg His Gly Asp Ala Thr Asp Val Arg
W--> 86 Gly
W--> 87 55 60 65
E--> 89 atc att cag aag ata gtg gac agt cac aaa gta aag cat gtg gcc
90 tgc 478
91 Ile Ile Gln Lys Ile Val Asp Ser His Lys Val Lys His Val Ala
W--> 92 Cys
W--> 93 70 75 80
E--> 95 tat gga ttc cgc ctc agt cac ctg cgg tca gag gag gtt cac tgg
96 ctt 526
97 Tyr Gly Phe Arg Leu Ser His Leu Arg Ser Glu Glu Val His Trp
W--> 98 Leu
W--> 99 85 90 95
E--> 101 cac gtg gat atg ggc gtc tcc agt gtg agg gag aag tat gag ctt
102 gct 574
103 His Val Asp Met Gly Val Ser Ser Val Arg Glu Lys Tyr Glu Leu
W--> 104 Ala
W--> 105 100 105 110
E--> 107 cac cca cca gag gag tgg aaa tat gaa ttg aga att cgt tat ttg
108 cca 622
109 His Pro Pro Glu Glu Trp Lys Tyr Glu Leu Arg Ile Arg Tyr Leu
W--> 110 Pro
W--> 111 115 120 125
E--> 112 130
E--> 114 aaa gga ttt cta aac cag ttt act gaa gat aag cca act ttg aat
115 ttc 670
116 Lys Gly Phe Leu Asn Gln Phe Thr Glu Asp Lys Pro Thr Leu Asn
W--> 117 Phe
W--> 118 135 140 145
E--> 120 ttc tat caa cag gtg aag agc gat tat atg tta gag ata gct gat
121 caa 718
122 Phe Tyr Gln Gln Val Lys Ser Asp Tyr Met Leu Glu Ile Ala Asp
W--> 123 Gln
W--> 124 150 155 160

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Input Set : A:\isph-533.seq.asc
Output Set: N:\CRF3\02052001\I757100.raw

E--> 126 gtg gac cag gaa att gct ttg aag ttg ggt tgt cta gaa ata cgg
127 cga 766
128 Val Asp Gln Glu Ile Ala Leu Lys Leu Gly Cys Leu Glu Ile Arg
W--> 129 Arg
W--> 130 165 170 175
E--> 132 tca tac tgg gag atg cgg ggc aat gca cta gaa aag aag tct aac
133 tat 814
134 Ser Tyr Trp Glu Met Arg Gly Asn Ala Leu Glu Lys Lys Ser Asn
W--> 135 Tyr
W--> 136 180 185 190
E--> 138 gaa gta tta gaa aaa gat gtt ggt tta aag cga ttt ttt cct aag
139 agt 862
140 Glu Val Leu Glu Lys Asp Val Gly Leu Lys Arg Phe Phe Pro Lys
W--> 141 Ser
W--> 142 195 200 205
E--> 143 210
E--> 145 tta ctg gat tct gtc aag gcc aaa aca cta aga aaa ctg atc caa
146 caa 910
147 Leu Leu Asp Ser Val Lys Ala Lys Thr Leu Arg Lys Leu Ile Gln
W--> 148 Gln
W--> 149 215 220 225
E--> 151 aca ttt aga caa ttt gcc aac ctt aat aga gaa gaa agt att ctg
152 aaa 958
153 Thr Phe Arg Gln Phe Ala Asn Leu Asn Arg Glu Glu Ser Ile Leu
W--> 154 Lys
W--> 155 230 235 240
E--> 157 ttc ttt gag atc ctg tct cca gtc tac aga ttt gat aag gaa tgc
158 ttc 1006
159 Phe Phe Glu Ile Leu Ser Pro Val Tyr Arg Phe Asp Lys Glu Cys
W--> 160 Phe
W--> 161 245 250 255
E--> 163 aag tgt gct ctt ggt tca agc tgg att att tca gtg gaa ctg gca
164 atc 1054
165 Lys Cys Ala Leu Gly Ser Ser Trp Ile Ile Ser Val Glu Leu Ala
W--> 166 Ile
W--> 167 260 265 270
E--> 169 ggc cca gaa gaa gga atc agt tac cta acg gac aag ggc tgc aat
170 ccc 1102
171 Gly Pro Glu Glu Gly Ile Ser Tyr Leu Thr Asp Lys Gly Cys Asn
W--> 172 Pro
W--> 173 275 280 285
E--> 174 290
E--> 176 aca cat ctt gct gac ttc act caa gtg caa acc att cag tat tca
177 aac 1150
178 Thr His Leu Ala Asp Phe Thr Gln Val Gln Thr Ile Gln Tyr Ser
W--> 179 Asn
W--> 180 295 300 305
E--> 182 agt gaa gac aag gac aga aaa gga atg cta caa cta aaa ata gca
183 ggt 1198

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DATE: 02/05/2001

TIME: 14:24:27

Input Set : A:\isph-533.seq.asc

Output Set: N:\CRF3\02052001\I757100.raw

184 Ser Glu Asp Lys Asp Arg Lys Gly Met Leu Gln Leu Lys Ile Ala
W--> 185 Gly
W--> 186 310 315 320
E--> 188 gca ccc gag cct ctg aca gtg acg gca cca tcc cta acc att gcg
189 gag 1246
190 Ala Pro Glu Pro Leu Thr Val Thr Ala Pro Ser Leu Thr Ile Ala
W--> 191 Glu
W--> 192 325 330 335
E--> 194 aat atg gct gac cta ata gat ggg tac tgc cgg ctg gtg aat gga
195 acc 1294
196 Asn Met Ala Asp Leu Ile Asp Gly Tyr Cys Arg Leu Val Asn Gly
W--> 197 Thr
W--> 198 340 345 350
E--> 200 tcg cag tca ttt atc atc aga cct cag aaa gaa ggt gaa cgg gct
201 ttg 1342
202 Ser Gln Ser Phe Ile Ile Arg Pro Gln Lys Glu Gly Glu Arg Ala
W--> 203 Leu
W--> 204 355 360 365
E--> 205 370
E--> 207 cca tca ata cca aag ttg gcc aac agc gaa aag caa ggc atg cgg
208 aca 1390
209 Pro Ser Ile Pro Lys Leu Ala Asn Ser Glu Lys Gln Gly Met Arg
W--> 210 Thr
W--> 211 375 380 385
E--> 213 cac gcc gtc tct gtg tca gaa aca gat gat tat gct gag att ata
214 gat 1438
215 His Ala Val Ser Val Ser Glu Thr Asp Asp Tyr Ala Glu Ile Ile
W--> 216 Asp
W--> 217 390 395 400
E--> 219 gaa gaa gat act tac acc atg ccc tca acc agg gat tat gag att
220 caa 1486
221 Glu Glu Asp Thr Tyr Thr Met Pro Ser Thr Arg Asp Tyr Glu Ile
W--> 222 Gln
W--> 223 405 410 415
E--> 225 aga gaa aga ata gaa ctt gga cga tgt att gga gaa ggc caa ttt
226 gga 1534
227 Arg Glu Arg Ile Glu Leu Gly Arg Cys Ile Gly Glu Gly Gln Phe
W--> 228 Gly
W--> 229 420 425 430
E--> 231 gat gta cat caa ggc att tat atg agt cca gag aat cca gct ttg
232 gcg 1582
233 Asp Val His Gln Gly Ile Tyr Met Ser Pro Glu Asn Pro Ala Leu
W--> 234 Ala
W--> 235 435 440 445
E--> 236 450
E--> 238 gtt gca att aaa aca tgt aaa aac tgt act tcg gac agc gtg aga
239 gag 1630
240 Val Ala Ile Lys Thr Cys Lys Asn Cys Thr Ser Asp Ser Val Arg
W--> 241 Glu

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Input Set : A:\isph-533.seq.asc
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W--> 242          455          460          465
E--> 244 aaa ttt ctt caa gaa gcc tta aca atg cgt cag ttt gac cat cct
      245 cat 1678
      246 Lys Phe Leu Gln Glu Ala Leu Thr Met Arg Gln Phe Asp His Pro
W--> 247 His
W--> 248          470          475          480
E--> 250 att gtg aag ctg att gga gtc atc aca gag aat cct gtc tgg ata
      251 atc 1726
      252 Ile Val Lys Leu Ile Gly Val Ile Thr Glu Asn Pro Val Trp Ile
W--> 253 Ile
W--> 254          485          490          495
E--> 256 atg gag ctg tgc aca ctt gga gag ctg agg tca ttt ttg caa gta
      257 agg 1774
      258 Met Glu Leu Cys Thr Leu Gly Glu Leu Arg Ser Phe Leu Gln Val
W--> 259 Arg
W--> 260          500          505          510
E--> 262 aaa tac agt ttg gat cta gca tct ttg atc ctg tat gcc tat cag
      263 ctt 1822
      264 Lys Tyr Ser Leu Asp Leu Ala Ser Leu Ile Leu Tyr Ala Tyr Gln
W--> 265 Leu
W--> 266 515          520          525
E--> 267 530
E--> 269 agt aca gct ctt gca tat cta gag agc aaa aga ttt gta cac agg
      270 gac 1870
      271 Ser Thr Ala Leu Ala Tyr Leu Glu Ser Lys Arg Phe Val His Arg
W--> 272 Asp
W--> 273          535          540          545
E--> 275 att gct gct cgg aat gtt ctg gtg tcc tca aat gat tgt gta aaa
      276 tta 1918
      277 Ile Ala Ala Arg Asn Val Leu Val Ser Ser Asn Asp Cys Val Lys
W--> 278 Leu
W--> 279          550          555          560
E--> 281 gga gac ttt gga tta tcc cga tat atg gaa gat agt act tac tac
      282 aaa 1966
      283 Gly Asp Phe Gly Leu Ser Arg Tyr Met Glu Asp Ser Thr Tyr Tyr
W--> 284 Lys
W--> 285          565          570          575
E--> 286 gct tcc aaa gga aaa ttg cct att aaa tgg atg gct cca gag tca
      287 atc 2014
      288 Ala Ser Lys Gly Lys Leu Pro Ile Lys Trp Met Ala Pro Glu Ser
W--> 289 Ile
W--> 290          580          585          590
E--> 292 aat ttt cga cgt ttt acc tca gct agt gac gta tgg atg ttt ggt
      293 gtg 2062
      294 Asn Phe Arg Arg Phe Thr Ser Ala Ser Asp Val Trp Met Phe Gly
W--> 295 Val
W--> 296 595          600          605
E--> 297 610
E--> 299 tgt atg tgg gag ata ctg atg cat ggt gtg aag cct ttt caa gga

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text

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Input Set : A:\isph-533.seq.asc

Output Set: N:\CRF3\02052001\I757100.raw

300 gtg 2110
301 Cys Met Trp Glu Ile Leu Met His Gly Val Lys Pro Phe Gln Gly
W--> 302 Val
W--> 303 615 620 625
E--> 305 aag aac aat gat gta atc ggt cga att gaa aat ggg gaa aga tta
306 cca 2158
307 Lys Asn Asn Asp Val Ile Gly Arg Ile Glu Asn Gly Glu Arg Leu
W--> 308 Pro
W--> 309 630 635 640
E--> 311 atg cct cca aat tgt cct cct acc ctg tac agc ctt atg acg aaa
312 tgc 2206
313 Met Pro Pro Asn Cys Pro Pro Thr Leu Tyr Ser Leu Met Thr Lys
W--> 314 Cys
W--> 315 645 650 655
E--> 317 tgg gcc tat gac ccc agc agg cgg ccc agg ttt act gaa ctt aaa
318 gct 2254
319 Trp Ala Tyr Asp Pro Ser Arg Arg Pro Arg Phe Thr Glu Leu Lys
W--> 320 Ala
W--> 321 660 665 670
E--> 323 cag ctg agc aca atc ctg gag gaa gag aag gct cag caa gaa gag
324 cgc 2302
325 Gln Leu Ser Thr Ile Leu Glu Glu Glu Lys Ala Gln Gln Glu Glu
W--> 326 Arg
W--> 327 675 680 685
E--> 328 690
E--> 330 atg agg atg gag tcc aga aga cag gcc aca gtg tcc tgg gac tcc
331 gga 2350
332 Met Arg Met Glu Ser Arg Arg Gln Ala Thr Val Ser Trp Asp Ser
W--> 333 Gly
W--> 334 695 700 705
E--> 336 ggg tct gat gaa gca cgc ccc aag ccc agc aga ccg ggt tat ccc
337 agt 2398
338 Gly Ser Asp Glu Ala Pro Pro Lys Pro Ser Arg Pro Gly Tyr Pro
W--> 339 Ser
W--> 340 710 715 720
E--> 342 ccg agg tcc agc gaa gga ttt tat ccc agc cca cag cac atg gta
343 caa 2446
344 Pro Arg Ser Ser Glu Gly Phe Tyr Pro Ser Pro Gln His Met Val
W--> 345 Gln
W--> 346 725 730 735
E--> 348 acc aat cat tac cag gtt tct ggc tac cct ggt tca cat gga atc
349 aca 2494
350 Thr Asn His Tyr Gln Val Ser Gly Tyr Pro Gly Ser His Gly Ile
W--> 351 Thr
W--> 352 740 745 750
E--> 354 gcc atg gct ggc agc atc tat cca ggt cag gca tct ctt ttg gac
355 caa 2542
356 Ala Met Ala Gly Ser Ile Tyr Pro Gly Gln Ala Ser Leu Leu Asp
W--> 357 Gln

Wrapped
text

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Input Set : A:\isph-533.seq.asc
 Output Set: N:\CRF3\02052001\I757100.raw

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W--> 358 755                      760                      765
E--> 359 770
E--> 361 aca gat tca tgg aat cat aga cct cag gag ata gca atg tgg cag
      362 ccc 2590
      363 Thr Asp Ser Trp Asn His Arg Pro Gln Glu Ile Ala Met Trp Gln
W--> 364 Pro
W--> 365                      775                      780                      785
E--> 367 aat gtg gag gac tct aca gta ttg gac ctg cga ggg att ggg caa
      368 gtg 2638
      369 Asn Val Glu Asp Ser Thr Val Leu Asp Leu Arg Gly Ile Gly Gln
W--> 370 Val
W--> 371                      790                      795                      800
E--> 373 ttg cca acc cat ctg atg gaa gag cgt cta atc cga cag caa cag
      374 gaa 2686
      375 Leu Pro Thr His Leu Met Glu Glu Arg Leu Ile Arg Gln Gln Gln
W--> 376 Glu
W--> 377                      805                      810                      815
E--> 379 atg gaa gaa gat cag cgc tgg ctg gaa aaa gag gaa aga ttt ctg
      380 aaa 2734
      381 Met Glu Glu Asp Gln Arg Trp Leu Glu Lys Glu Glu Arg Phe Leu
W--> 382 Lys
W--> 383                      820                      825                      830
E--> 385 cct gat gtg aga ctc tct cga ggc agt att gac agg gag gat gga
      386 agt 2782
      387 Pro Asp Val Arg Leu Ser Arg Gly Ser Ile Asp Arg Glu Asp Gly
W--> 388 Ser
W--> 389 835                      840                      845
E--> 390 850
E--> 392 ctt cag ggt ccg att gga aac caa cat ata tat cag cct gtg ggt
      393 aaa 2830
      394 Leu Gln Gly Pro Ile Gly Asn Gln His Ile Tyr Gln Pro Val Gly
W--> 395 Lys
W--> 396                      855                      860                      865
E--> 398 cca gat cct gca gct cca cca aag aaa ccg cct cgc cct gga gct
      399 ccc 2878
      400 Pro Asp Pro Ala Ala Pro Pro Lys Lys Pro Pro Arg Pro Gly Ala
W--> 401 Pro
W--> 402                      870                      875                      880
E--> 404 ggt cat ctg gga agc ctt gcc agc ctc agc agc cct gct gac agc
      405 tac 2926
      406 Gly His Leu Gly Ser Leu Ala Ser Leu Ser Ser Pro Ala Asp Ser
W--> 407 Tyr
W--> 408                      885                      890                      895
E--> 410 aac gag ggt gtc aag ctt cag ccc cag gaa atc agc ccc cct cct
      411 act 2974
      412 Asn Glu Gly Val Lys Leu Gln Pro Gln Glu Ile Ser Pro Pro Pro
W--> 413 Thr
W--> 414                      900                      905                      910
E--> 416 gcc aac ctg gac cgg tcg aat gat aag gtg tac gag aat gtg acg

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*wrapped
text*

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PATENT APPLICATION: US/09/757,100

DATE: 02/05/2001
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Input Set : A:\isph-533.seq.asc
Output Set: N:\CRF3\02052001\I757100.raw

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417 ggc 3022
418 Ala Asn Leu Asp Arg Ser Asn Asp Lys Val Tyr Glu Asn Val Thr
W--> 419 Gly
W--> 420 915 920 925
E--> 421 930
E--> 423 ctg gtg aaa gct gtc atc gag atg tcc agt aaa atc cag cca gcc
424 cca 3070
425 Leu Val Lys Ala Val Ile Glu Met Ser Ser Lys Ile Gln Pro Ala
W--> 426 Pro
W--> 427 935 940 945
E--> 429 cca gag gag tat gtc cct atg gtg aag gaa gtc ggc ttg gcc ctg
430 agg 3118
431 Pro Glu Glu Tyr Val Pro Met Val Lys Glu Val Gly Leu Ala Leu
W--> 432 Arg
W--> 433 950 955 960
E--> 435 aca tta ttg gcc act gtg gat gag acc att ccc ctc cta cca gcc
436 agc 3166
437 Thr Leu Leu Ala Thr Val Asp Glu Thr Ile Pro Leu Leu Pro Ala
W--> 438 Ser
W--> 439 965 970 975
E--> 441 acc cac cga gag att gag atg gca cag aag cta ttg aac tct gac
442 ctg 3214
443 Thr His Arg Glu Ile Glu Met Ala Gln Lys Leu Leu Asn Ser Asp
W--> 444 Leu
W--> 445 980 985 990
E--> 447 ggt gag ctc atc aac aag atg aaa ctg gcc cag cag tat gtc atg
448 acc 3262
449 Gly Glu Leu Ile Asn Lys Met Lys Leu Ala Gln Gln Tyr Val Met
W--> 450 Thr
W--> 451 995 1000 1005
E--> 452 1010
E--> 454 agc ctc cag caa gag tac aaa aag caa atg ctg act gct gct cac
455 gcc 3310
456 Ser Leu Gln Gln Glu Tyr Lys Lys Gln Met Leu Thr Ala Ala His
W--> 457 Ala
W--> 458 1015 1020 1025
E--> 460 ctg gct gtg gat gcc aaa aac tta ctc gat gtc att gac caa gca
461 aga 3358
462 Leu Ala Val Asp Ala Lys Asn Leu Leu Asp Val Ile Asp Gln Ala
W--> 463 Arg
W--> 464 1030 1035 1040
E--> 466 ctg aaa atg ctt ggg cag acg aga cca cac tga gcctccccta
467 ggagcacgtc 3411
468 Leu Lys Met Leu Gly Gln Thr Arg Pro His
W--> 469 1045 1050
E--> 471 ttgctaccct cttttgaaga tgttctctag ccttccacca gcagcgagga
472 attaaccttg 3471
E--> 474 tgtcctcagt cgccagcact tacagctcca acttttttga atgaccatct
475 ggttgaaaaa 3531
```

Wrapped
text

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/757,100
 DATE: 02/05/2001
 TIME: 14:24:27

Input Set : A:\isph-533.seq.asc
 Output Set: N:\CRF3\02052001\I757100.raw

```

E--> 477 tctttctcat   ataagtttaa   ccacactttg   atttgggttc   attttttgtt
      478 ttgttttttt 3591
E--> 480 caatcatgat   attcagaaaa   atccaggatc   caaaatgttg   cgtttttcta
      481 agaattgaaaa 3651
E--> 483 ttatatgttaa   gctttttaagc   atcatgaaga   acaatttatg   ttcacattaa
      484 gatacgttct 3711
E--> 486 aaaggggggat   ggccaagggg   tgacatctta   attcctaaac   taccttagct
      487 gcatagtqqa 3771
E--> 489 agaggagagc                                tagaagcaaa
      490 3791
      493 <210> SEQ ID NO: 2
      494 <211> LENGTH: 1052
      495 <212> TYPE: PRT
      496 <213> ORGANISM: Homo sapiens
      498 <400> SEQUENCE: 2
      499 Met Ala Ala Ala Tyr Leu Asp Pro Asn Leu Asn His Thr Pro Asn
E--> 500 Ser
E--> 501 1 5 10 15
      503 Ser Thr Lys Thr His Leu Gly Thr Gly Met Glu Arg Ser Pro Gly
E--> 504 Ala
E--> 505 20 25 30
      507 Met Glu Arg Val Leu Lys Val Phe His Tyr Phe Glu Ser Asn Ser
E--> 508 Glu
E--> 509 35 40 45
      511 Pro Thr Thr Trp Ala Ser Ile Ile Arg His Gly Asp Ala Thr Asp
E--> 512 Val
E--> 513 50 55 60
      515 Arg Gly Ile Ile Gln Lys Ile Val Asp Ser His Lys Val Lys His
E--> 516 Val
E--> 517 65 70 75
E--> 518 80
      520 Ala Cys Tyr Gly Phe Arg Leu Ser His Leu Arg Ser Glu Glu Val
E--> 521 His
E--> 522 85 90 95
      524 Trp Leu His Val Asp Met Gly Val Ser Ser Val Arg Glu Lys Tyr
E--> 525 Glu
E--> 526 100 105 110
      528 Leu Ala His Pro Pro Glu Glu Trp Lys Tyr Glu Leu Arg Ile Arg
E--> 529 Tyr
E--> 530 115 120 125
      532 Leu Pro Lys Gly Phe Leu Asn Gln Phe Thr Glu Asp Lys Pro Thr
E--> 533 Leu
E--> 534 130 135 140
      536 Asn Phe Phe Tyr Gln Gln Val Lys Ser Asp Tyr Met Leu Glu Ile
E--> 537 Ala
E--> 538 145 150 155
E--> 539 160
      541 Asp Gln Val Asp Gln Glu Ile Ala Leu Lys Leu Gly Cys Leu Glu
E--> 542 Ile

```

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/757,100

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Input Set : A:\isph-533.seq.asc
Output Set: N:\CRF3\02052001\I757100.raw

E--> 543 165 170 175
545 Arg Arg Ser Tyr Trp Glu Met Arg Gly Asn Ala Leu Glu Lys Lys
E--> 546 Ser
E--> 547 180 185 190
549 Asn Tyr Glu Val Leu Glu Lys Asp Val Gly Leu Lys Arg Phe Phe
E--> 550 Pro
E--> 551 195 200 205
553 Lys Ser Leu Leu Asp Ser Val Lys Ala Lys Thr Leu Arg Lys Leu
E--> 554 Ile
E--> 555 210 215 220
557 Gln Gln Thr Phe Arg Gln Phe Ala Asn Leu Asn Arg Glu Glu Ser
E--> 558 Ile
E--> 559 225 230 235
E--> 560 240
562 Leu Lys Phe Phe Glu Ile Leu Ser Pro Val Tyr Arg Phe Asp Lys
E--> 563 Glu
E--> 564 245 250 255
566 Cys Phe Lys Cys Ala Leu Gly Ser Ser Trp Ile Ile Ser Val Glu
E--> 567 Leu
E--> 568 260 265 270
570 Ala Ile Gly Pro Glu Glu Gly Ile Ser Tyr Leu Thr Asp Lys Gly
E--> 571 Cys
E--> 572 275 280 285
574 Asn Pro Thr His Leu Ala Asp Phe Thr Gln Val Gln Thr Ile Gln
E--> 575 Tyr
E--> 576 290 295 300
578 Ser Asn Ser Glu Asp Lys Asp Arg Lys Gly Met Leu Gln Leu Lys
E--> 579 Ile
E--> 580 305 310 315
E--> 581 320
583 Ala Gly Ala Pro Glu Pro Leu Thr Val Thr Ala Pro Ser Leu Thr
E--> 584 Ile
E--> 585 325 330 335
587 Ala Glu Asn Met Ala Asp Leu Ile Asp Gly Tyr Cys Arg Leu Val
E--> 588 Asn
E--> 589 340 345 350
591 Gly Thr Ser Gln Ser Phe Ile Ile Arg Pro Gln Lys Glu Gly Glu
E--> 592 Arg
E--> 593 355 360 365
595 Ala Leu Pro Ser Ile Pro Lys Leu Ala Asn Ser Glu Lys Gln Gly
E--> 596 Met
E--> 597 370 375 380
599 Arg Thr His Ala Val Ser Val Ser Glu Thr Asp Asp Tyr Ala Glu
E--> 600 Ile
E--> 601 385 390 395
E--> 602 400
604 Ile Asp Glu Glu Asp Thr Tyr Thr Met Pro Ser Thr Arg Asp Tyr
E--> 605 Glu
E--> 606 405 410 415

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Input Set : A:\isph-533.seq.asc

Output Set: N:\CRF3\02052001\I757100.raw

608 Ile Gln Arg Glu Arg Ile Glu Leu Gly Arg Cys Ile Gly Glu Gly
E--> 609 Gln
E--> 610 420 425 430
612 Phe Gly Asp Val His Gln Gly Ile Tyr Met Ser Pro Glu Asn Pro
E--> 613 Ala
E--> 614 435 440 445
616 Leu Ala Val Ala Ile Lys Thr Cys Lys Asn Cys Thr Ser Asp Ser
E--> 617 Val
E--> 618 450 455 460
620 Arg Glu Lys Phe Leu Gln Glu Ala Leu Thr Met Arg Gln Phe Asp
E--> 621 His
E--> 622 465 470 475
E--> 623 480
625 Pro His Ile Val Lys Leu Ile Gly Val Ile Thr Glu Asn Pro Val
E--> 626 Trp
E--> 627 485 490 495
629 Ile Ile Met Glu Leu Cys Thr Leu Gly Glu Leu Arg Ser Phe Leu
E--> 630 Gln
E--> 631 500 505 510
633 Val Arg Lys Tyr Ser Leu Asp Leu Ala Ser Leu Ile Leu Tyr Ala
E--> 634 Tyr
E--> 635 515 520 525
637 Gln Leu Ser Thr Ala Leu Ala Tyr Leu Glu Ser Lys Arg Phe Val
E--> 638 His
E--> 639 530 535 540
641 Arg Asp Ile Ala Ala Arg Asn Val Leu Val Ser Ser Asn Asp Cys
E--> 642 Val
E--> 643 545 550 555
E--> 644 560
646 Lys Leu Gly Asp Phe Gly Leu Ser Arg Tyr Met Glu Asp Ser Thr
E--> 647 Tyr
E--> 648 565 570 575
650 Tyr Lys Ala Ser Lys Gly Lys Leu Pro Ile Lys Trp Met Ala Pro
E--> 651 Glu
E--> 652 580 585 590
654 Ser Ile Asn Phe Arg Arg Phe Thr Ser Ala Ser Asp Val Trp Met
E--> 655 Phe
E--> 656 595 600 605
658 Gly Val Cys Met Trp Glu Ile Leu Met His Gly Val Lys Pro Phe
E--> 659 Gln
E--> 660 610 615 620
662 Gly Val Lys Asn Asn Asp Val Ile Gly Arg Ile Glu Asn Gly Glu
E--> 663 Arg
E--> 664 625 630 635
E--> 665 640
666 Leu Pro Met Pro Pro Asn Cys Pro Pro Thr Leu Tyr Ser Leu Met
E--> 667 Thr
E--> 668 645 650 655
670 Lys Cys Trp Ala Tyr Asp Pro Ser Arg Arg Pro Arg Phe Thr Glu

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RAW SEQUENCE LISTING

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Input Set : A:\isph-533.seq.asc

Output Set: N:\CRF3\02052001\I757100.raw

E--> 671 Leu
E--> 672 660 665 670
674 Lys Ala Gln Leu Ser Thr Ile Leu Glu Glu Glu Lys Ala Gln Gln
E--> 675 Glu
E--> 676 675 680 685
678 Glu Arg Met Arg Met Glu Ser Arg Arg Gln Ala Thr Val Ser Trp
E--> 679 Asp
E--> 680 690 695 700
682 Ser Gly Gly Ser Asp Glu Ala Pro Pro Lys Pro Ser Arg Pro Gly
E--> 683 Tyr
E--> 684 705 710 715
E--> 685 720
687 Pro Ser Pro Arg Ser Ser Glu Gly Phe Tyr Pro Ser Pro Gln His
E--> 688 Met
E--> 689 725 730 735
691 Val Gln Thr Asn His Tyr Gln Val Ser Gly Tyr Pro Gly Ser His
E--> 692 Gly
E--> 693 740 745 750
695 Ile Thr Ala Met Ala Gly Ser Ile Tyr Pro Gly Gln Ala Ser Leu
E--> 696 Leu
E--> 697 755 760 765
699 Asp Gln Thr Asp Ser Trp Asn His Arg Pro Gln Glu Ile Ala Met
E--> 700 Trp
E--> 701 770 775 780
703 Gln Pro Asn Val Glu Asp Ser Thr Val Leu Asp Leu Arg Gly Ile
E--> 704 Gly
E--> 705 785 790 795
E--> 706 800
708 Gln Val Leu Pro Thr His Leu Met Glu Glu Arg Leu Ile Arg Gln
E--> 709 Gln
E--> 710 805 810 815
712 Gln Glu Met Glu Glu Asp Gln Arg Trp Leu Glu Lys Glu Glu Arg
E--> 713 Phe
E--> 714 820 825 830
716 Leu Lys Pro Asp Val Arg Leu Ser Arg Gly Ser Ile Asp Arg Glu
E--> 717 Asp
E--> 718 835 840 845
720 Gly Ser Leu Gln Gly Pro Ile Gly Asn Gln His Ile Tyr Gln Pro
E--> 721 Val
E--> 722 850 855 860
724 Gly Lys Pro Asp Pro Ala Ala Pro Pro Lys Lys Pro Pro Arg Pro
E--> 725 Gly
E--> 726 865 870 875
E--> 727 880
729 a Pro Gly His Leu Gly Ser Leu Ala Ser Leu Ser Ser Pro Ala
E--> 730 Asp
E--> 731 885 890 895
733 Ser Tyr Asn Glu Gly Val Lys Leu Gln Pro Gln Glu Ile Ser Pro
E--> 734 Pro

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text

RAW SEQUENCE LISTING DATE: 02/05/2001
 PATENT APPLICATION: US/09/757,100 TIME: 14:24:27

Input Set : A:\isph-533.seq.asc
 Output Set: N:\CRF3\02052001\I757100.raw

```

E--> 735          900          905          910
      737 Pro Thr Ala Asn Leu Asp Arg Ser Asn Asp Lys Val Tyr Glu Asn
E--> 738 Val
E--> 739          915          920          925
      741 Thr Gly Leu Val Lys Ala Val Ile Glu Met Ser Ser Lys Ile Gln
E--> 742 Pro
E--> 743          930          935          940
      745 Ala Pro Pro Glu Glu Tyr Val Pro Met Val Lys Glu Val Gly Leu
E--> 746 Ala
E--> 747 945          950          955
E--> 748 960
      750 Leu Arg Thr Leu Leu Ala Thr Val Asp Glu Thr Ile Pro Leu Leu
E--> 751 Pro
E--> 752          965          970          975
      754 Ala Ser Thr His Arg Glu Ile Glu Met Ala Gln Lys Leu Leu Asn
E--> 755 Ser
E--> 756          980          985          990
      757 Asp Leu Gly Glu Leu Ile Asn Lys Met Lys Leu Ala Gln Gln Tyr
E--> 758 Val
E--> 759          995          1000          1005
      761 Met Thr Ser Leu Gln Gln Glu Tyr Lys Lys Gln Met Leu Thr Ala
E--> 762 Ala
E--> 763          1010          1015          1020
      765 His Ala Leu Ala Val Asp Ala Lys Asn Leu Leu Asp Val Ile Asp
E--> 766 Gln
E--> 767 025          1030          1035
E--> 768 1040
      770 Ala Arg Leu Lys Met Leu Gly Gln Thr Arg Pro His
E--> 771          1045          1050
      774 <210> SEQ ID NO: 3
      775 <211> LENGTH: 20
      776 <212> TYPE: DNA
      777 <213> ORGANISM: Artificial Sequence
      779 <220> FEATURE:
      780 <223> OTHER INFORMATION: antisense sequence
      782 <400> SEQUENCE: 3
E--> 783 ccgcgggctc          acagtggctc
      784 20
      787 <210> SEQ ID NO: 4
      788 <211> LENGTH: 20
      789 <212> TYPE: DNA
      790 <213> ORGANISM: Artificial Sequence
      792 <220> FEATURE:
      793 <223> OTHER INFORMATION: antisense sequence
      795 <400> SEQUENCE: 4
E--> 796 ggcgccgtga          agcgaaggca
      797 20
      800 <210> SEQ ID NO: 5
      801 <211> LENGTH: 20

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VERIFICATION SUMMARY

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TIME: 14:24:29

Input Set : A:\isph-533.seq.asc

Output Set: N:\CRF3\02052001\I757100.raw

L:16 M:270 C: Current Application Number differs, Replaced Application Number
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:43 M:285 W: Invalid Journal Date: Wrong YYYY-MM-DD,MMM-YYYY or SEASON-YYYY, Wrong Journal Date:YYYY-MM-DD,MMM-YYYY or Season-YYYY
L:48 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:1
M:254 Repeated in SeqNo=1
L:67 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:68 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:73 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:74 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:79 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:80 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:86 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:87 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:92 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:93 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:98 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:99 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:110 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:117 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:129 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:130 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:135 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:136 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:141 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:148 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:149 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:154 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:155 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:160 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:161 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:166 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:172 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:173 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:179 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:180 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:185 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:186 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:191 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:192 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:197 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

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Input Set : A:\isph-533.seq.asc

Output Set: N:\CRF3\02052001\I757100.raw

L:198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:203 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:204 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:210 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:211 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:216 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:217 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:500 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:783 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:3
L:796 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:4
L:809 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:5
L:822 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:6
L:830 M:283 W: Missing Blank Line separator, <220> field identifier
L:834 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:7
L:847 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:8
L:860 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:9
L:873 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:10
L:886 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:11
L:899 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:12
L:911 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:13
L:924 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:14
L:937 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:15
L:950 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:16
L:963 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:17
L:971 M:283 W: Missing Blank Line separator, <220> field identifier
L:975 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:18
L:988 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:19
L:1001 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:20
L:1014 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:21
L:1027 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:22
L:1040 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:23
L:1052 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:24
L:1065 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:25
L:1078 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:26
L:1091 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:27
L:1104 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:28
L:1112 M:283 W: Missing Blank Line separator, <220> field identifier
L:1116 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:29
L:1129 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:30
L:1142 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:31
L:1155 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:32
L:1168 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:33
L:1181 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:34
L:1193 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:35
L:1206 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:36
L:1219 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:37
L:1232 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:38
L:1245 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:39

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Input Set : A:\isph-533.seq.asc

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L:1253 M:283 W: Missing Blank Line separator, <220> field identifier
L:1257 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:40
L:1270 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:41
L:1283 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:42
L:1295 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:43
L:1311 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:1311 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:44